

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/805694

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 04/05/2001
 PATENT APPLICATION: US/09/805,694 TIME: 08:05:50

Input Set : A:\BB1432 US NA Seq Listing.txt
 Output Set: N:\CRF3\04052001\I805694.raw

**Does Not Comply
 Corrected Diskette Needed**

3 <110> APPLICANT: Kinney, Anthony
 5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
 7 <130> FILE REFERENCE: BB1432 US NA
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/805,694
 C--> 10 <141> CURRENT FILING DATE: 2001-03-14
 12 <150> PRIOR APPLICATION NUMBER: 60/189,823
 W--> 13 <151> PRIOR FILING DATE: 16 MARCH 2000 2000-03-16
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: Microsoft Office 97

ERRORED SEQUENCES

230 <210> SEQ ID NO: 5
 231 <211> LENGTH: 494
 232 <212> TYPE: DNA
 233 <213> ORGANISM: Glycine max
 235 <400> SEQUENCE: 5
 E--> 236 acacagctng cacatattac atacacgtga atcactaatt aagccatgga gaagaaatca 60
 237 atagctgggt tgtgcttcct ctctcttggt ctctttgttg ctcaagaagt tgtggtgcaa 120
 238 actgaggcaa agacttgca gaacctggct gatacataga ggggtccatg cttcaccact 180
 239 ggcagctgcy atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac 240
 240 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300
 241 agatgcatgc agcgctattt tataaaaaat acaactacta tatactatat ataataagac 360
 E--> 242 tgggcgctgc atcaatgacc ctatgtanta ttttatatat tattaccgat gtcaagaact 420
 E--> 243 atagatgcat gtactgtgca taacggctga gttatgtccn tagttanga ataaaaataa 480
 244 agtgcgttg ttgc 494

*see item 10
 on Enr
 Summary sheet*

VERIFICATION SUMMARY DATE: 04/05/2001
PATENT APPLICATION: US/09/805,694 TIME: 08:05:52

Input Set : A:\BB1432 US NA Seq Listing.txt
Output Set: N:\CRF3\04052001\I805694.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:236 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
M:340 Repeated in SeqNo=5